

## SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is primate DIRS1 nucleotide sequence.  
SEQ ID NO: 2 is primate DIRS1 polypeptide sequence.  
SEQ ID NO: 3 is primate DIRS2 nucleotide sequence.  
SEQ ID NO: 4 is primate DIRS2 polypeptide sequence.  
SEQ ID NO: 5 is primate IFNY receptor subunit beta polypeptide sequence.  
10 SEQ ID NO: 6 is primate CRF2-4 receptor subunit polypeptide sequence.

## (1) GENERAL INFORMATION:

15 (i) APPLICANT: Parham, Christi L.  
Moore, Kevin W.  
Murgolo, Nicholas J.  
Bazan, J. Fernando

20 (ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related  
Reagents and Methods

(iii) NUMBER OF SEQUENCES: 6

25 (iv) CORRESPONDENCE ADDRESS:  
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(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
35 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

40 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE: 08-MAR-1999  
(C) CLASSIFICATION:

45 (viii) ATTORNEY/AGENT INFORMATION:  
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(C) REFERENCE/DOCKET NUMBER: DX0804K

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## (2) INFORMATION FOR SEQ ID NO:1:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1381 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- 10 (B) LOCATION: 132..1064

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 567
- 15 (D) OTHER INFORMATION: /note= "nucleotides 567, 573, 1336, 1342, and 1369 designated C, but each may be A, C, G, or T"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- 20 (B) LOCATION: 643
- (D) OTHER INFORMATION: /note= "nucleotides 643, 1287, and 1290 designated C, but each may be C or G"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 772
- 25 (D) OTHER INFORMATION: /note= "nucleotides 772, 806, and 1261 designated G, but each may be A or G"

30 (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1236
- (D) OTHER INFORMATION: /note= "nucleotides 1236, 1260, 1282, and 1289 are designated T, but each may be G or T"

35 (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1247
- 40 (D) OTHER INFORMATION: /note= "nucleotides 1247, 1257, 1293, and 1302 designated C, but each may be C or T"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1266
- 45 (D) OTHER INFORMATION: /note= "nucleotides 1266 and 1298 designated T, but each may be A or T"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACCCACG CGTCCGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA	60
AGATGGCTGA GATGGACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAAC	120
55 GAGTCTACCA A ATG CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA	170

		Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr				
		1					5					10						
5		AGT	CTT	TTC	ATG	TGG	TTT	TTC	TAC	GCA	TTG	ATT	CCA	TGT	TTG	CTC	ACA	218
		Ser	Leu	Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	
		15							20					25				
10		GAT	GAA	GTG	GCC	ATT	CTG	CCT	GCC	CCT	CAG	AAC	CTC	TCT	GTA	CTC	TCA	266
		Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
		30						35				40			45			
		ACC	AAC	ATG	AAG	CAT	CTC	TTG	ATG	TGG	AGC	CCA	GTG	ATC	GCG	CCT	GGA	314
		Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly	
		50							55				60					
15		GAA	ACA	GTG	TAC	TAT	TCT	GTC	GAA	TAC	CAG	GGG	GAG	TAC	GAG	AGC	CTG	362
		Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu	
		65							70				75					
20		TAC	ACG	AGC	CAC	ATC	TGG	ATC	CCC	AGC	AGC	TGG	TGC	TCA	CTC	ACT	GAA	410
		Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu	
		80							85				90					
25		GGT	CCT	GAG	TGT	GAT	GTC	ACT	GAT	GAC	ATC	ACG	GCC	ACT	GTG	CCA	TAC	458
		Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr	
		95							100				105					
30		AAC	CTT	CGT	GTC	AGG	GCC	ACA	TTG	GGC	TCA	CAG	ACC	TCA	GCC	TGG	AGC	506
		Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser	
		110						115				120			125			
		ATC	CTG	AAG	CAT	CCC	TTT	AAT	AGA	AAC	TCA	ACC	ATC	CTT	ACC	CGA	CCT	554
		Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro	
		130							135				140					
35		GGG	ATG	GAG	ATC	CCC	AAA	CAT	GGC	TTC	CAC	CTG	GTT	ATT	GAG	CTG	GAG	602
		Gly	Met	Glu	Ile	Pro	Lys	His	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu	
		145							150				155					
40		GAC	CTG	GGG	CCC	CAG	TTT	GAG	TTC	CTT	GTG	GCC	TAC	TGG	ACG	AGG	GAG	650
		Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Thr	Arg	Glu	
		160							165				170					
45		CCT	GGT	GCC	GAG	GAA	CAT	GTC	AAA	ATG	GTG	AGG	AGT	GGG	GGT	ATT	CCA	698
		Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	
		175							180				185					
50		GTG	CAC	CTA	GAA	ACC	ATG	GAG	CCA	GGG	GCT	GCA	TAC	TGT	GTG	AAG	GCC	746
		Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	
		190							195				200				205	
		CAG	ACA	TTC	GTG	AAG	GCC	ATT	GGG	AGG	TAC	AGC	GCC	TTC	AGC	CAG	ACA	794
		Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	
		210								215				220				

	GAA TGT GTG GAG GTG CAA GGA GAG GCC ATT CCC CTG GTA CTG GCC CTG Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu 225 . . . . . 230 . . . . . 235	842
5	TTT GCC TTT GTT GGC TTC ATG CTG ATC CTT GTG GTC GTG CCA CTG TTC Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe 240 . . . . . 245 . . . . . 250	890
10	GTC TGG AAA ATG GGC CGG CTG CTC CAG TAC TCC TGT TGC CCC GTG GTG Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val 255 . . . . . 260 . . . . . 265	938
15	GTC CTC CCA GAC ACC TTG AAA ATA ACC AAT TCA CCC CAG AAG TTA ATC Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile 270 . . . . . 275 . . . . . 280 . . . . . 285	986
20	AGC TGC AGA AGG GAG GAG GTG GAT GCC TGT GCC ACG GCT GTG ATG TCT Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser 290 . . . . . 295 . . . . . 300	1034
25	CCT GAG GAA CTC CTC AGG GCC TGG ATC TCA TAGGTTGCG GAAGGGCCCA Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser 305 . . . . . 310	1084
30	GGTGAAGCCG AGAACCTGGT CTGCATGACA TGGAAACCAT GAGGGGACAA GTTGTGTTTC TGTTTTCCGC CACGGACAAG GGATGAGAGA AGTAGGAAGA GCCTGTTGTC TACAAGTCTA GAAGCAACCA TCAGAGGCAG GGTGGTTGT CTAACAGAAC AACTGACTGA GGCTATGGGG GTTGTGACCT CTAGACTTTG GGCTTCCACT TGCTTGGCTG AGCAACCCTG GGAAAAGTGA CTTCATCCCT TCGGTCCCAA GTTTCTCAT CTGTAATGGG GGATCCCTAC AAAACTG	1144 1204 1264 1324 1381
35	(2) INFORMATION FOR SEQ ID NO:2:	

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe 1 . . . . . 5 . . . . . 10 . . . . . 15
50	Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val 20 . . . . . 25 . . . . . 30
	Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met 35 . . . . . 40 . . . . . 45

	Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val			
	50	55	60	
	Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser			
5	65	70	75	80
	His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu			
	85	90	95	
10	Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg			
	100	105	110	
	Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys			
	115	120	125	
15	His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu			
	130	135	140	
20	Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly			
	145	150	155	160
	Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu Pro Gly Ala			
	165	170	175	
25	Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu			
	180	185	190	
	Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe			
	195	200	205	
30	Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val			
	210	215	220	
35	Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe			
	225	230	235	240
	Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys			
	245	250	255	
40	Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro			
	260	265	270	
	Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg			
	275	280	285	
45	Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu			
	290	295	300	
50	Leu Leu Arg Ala Trp Ile Ser			
	305	310		

(2) INFORMATION FOR SEQ ID NO:3:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1244 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- 10 (B) LOCATION: 2..694

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 193
- 15 (D) OTHER INFORMATION: /note= "nucleotide 193 designated C, may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	C CGG GTC GAC CCA CGC GTC CGC CTG GTT TCC CCC TGG CTG ACA GTG Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val	46
	1 5 10 15	
25	CCT TGG TTC CTG TCC TGT TGG AAT GTT ACC ATT GGG CCT CCT GAG AGC Pro Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser	94
	20 25 30	
30	ATC TGG GTG ACG CCG GGA GAA GCC TCC CTC ATC ATC AGG TTC TCC TCT Ile Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser	142
	35 40 45	
35	CCC TTC GAC GTC CCT CCC AAC CTG GGC TAT TTC CAG TAC TAT GTC CAT Pro Phe Asp Val Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His	190
	50 55 60	
40	TAC TGG GAA AAG GCG GGA ATC CAA AAG GTT AAA GGT CCT TTC AAG AGC Tyr Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser	238
	65 70 75	
45	AAC TCC ATC GTG TTG GAT GGC TTG AGA CCC TTA AGA GAA TAC TGT TTA Asn Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu	286
	80 85 90 95	
50	100 105 110	
55	GGC CGC TTA AGC AAC ATA ACT TGC TAC GAA ACA ATG ATG GAT GCC ACT Gly Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr	382
	115 120 125	
55	130 135 140	430

	CTG GCG GCG CTG GCG GGG GGC TGT TTC TTC CTG GTG CTG AGA TAC AAA	478
	Leu Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys	
145	150	155
5	GGC CTG GTG AAA TAC TGG TTT CAC TCT CCG CCA AGC ATC CCA TCA CAA	526
	Gly Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln	
160	165	170
	175	
10	ATC GAA GAG TAT CTG AAG GAC CCG AGC CAG CCT ATC CTA GAG GCC CTG	574
	Ile Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu	
	180	185
	190	
15	GAC AAG GAC ACG TCA CCA ACA GAT GAT GCC TGG GAC TTG GTG TCT GTT	622
	Asp Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val	
	195	200
	205	
20	GTT GCA TTT CCA GCA AAG GAG CAA GAA GAT GTT CCC CAA AGC ACT TTG	670
	Val Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu	
	210	215
	220	
	ACC CAA AAC TCT GGT GCG GTC TGC TAGCCTGTGG GGTAAGGGCT CTGAGCCGAG	724
	Thr Gln Asn Ser Gly Ala Val Cys	
	225	230
25	GAAGCTGCTG ATGTCCATGT CAGCACTTTA TGGAAATCCGG TCCTCCATTG TCCTGTCCCC	784
	AAAAGGCCCG TCAGTGCCTG TGAAGATGTA ACGGGTCTCA TGGGGGCGAC AAGCTTATTG	844
30	ATTTTTTCT TCAAACTAAG AGTTTCTAA TCATACGCGT TTTTAGAATA ATTCTACAGA	904
	TATGTCCCCG AAAGATTAAG ATTTCTCTTA AACACTAAAA AGACATGTAA TTATTTGTTA	964
	GCAAATGGGC GTCTGGCACG CCTCTGACAC TTTTCGTCA GCAGCCAGGA CACGAGGTCC	1024
35	CCTCCTTGAT GAAGCCCCTC GGGCAGACCA TGTCACCTGT CCCAGCCTGC CCCAAGAAGG	1084
	GACATTAAGT GGCCCTTCTT CATATCCAAA CACCTGGCTT GAAATGTGAT TAGCCCTGTA	1144
40	AATAGTTCA CAGAGATTAAG GCCTTTTTT CCCCCAAGTT AGGAATAAAA GACTATAATT	1204
	AACTTTTAA AAAAAAAA AAAAAAAA AAAAAAAA	1244

45 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
1 5 10 15

5 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
20 25 30

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
35 40 45

10 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr  
50 55 60

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
65 70 75 80

15 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
85 90 95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
20 100 105 110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
115 120 125

25 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
130 135 140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
145 150 155 160

30 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
165 170 175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
35 180 185 190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
195 200 205

40 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
210 215 220

Gln Asn Ser Gly Ala Val Cys  
225 230

45 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 337 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe  
1 5 10 15

10 Ala Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala  
20 25 30

15 Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser  
35 40 45

20 Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg  
50 55 60

25 Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met  
65 70 75 80

30 Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe  
85 90 95

35 Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr  
100 105 110

40 Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr  
115 120 125

45 Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu  
130 135 140

50 Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser  
145 150 155 160

55 Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr  
165 170 175

60 Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe  
180 185 190

65 Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr  
195 200 205

70 Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe  
210 215 220

75 Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp  
225 230 235 240

80 Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe  
245 250 255

85 Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys  
260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro  
275 280 285

5 Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu  
290 295 300

10 Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val  
305 310 315 320

15 Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr  
325 330 335

Leu

15 (2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser  
1 5 10 15

35 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val  
20 25 30

40 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly  
35 40 45

45 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp  
50 55 60

55 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser  
65 70 75 80

65 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu  
85 90 95

50 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile  
100 105 110

55 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His  
115 120 125

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
130 135 140

5 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
145 150 155 160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
165 170 175

10 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
195 200 205

15 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala  
210 215 220

20 Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly  
225 230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe  
245 250 255

25 Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His  
260 265 270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu  
275 280 285

30 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser  
290 295 300

35 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly  
305 310 315 320

Gln Gly Pro Gln Ser  
325